Samβada: User manual

Sylvie Stucki and Stéphane Joost*

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*Laboratory of Geographic Information Systems (LASIG), School of Civil and Environmental Engineering (ENAC), Ecole Polytechnique Fédérale de Lausanne (EPFL), Bâtiment GC, Station 18, 1015 Lausanne, Switzerland
Webpage: `lasig.epfl.ch/sambada`
Contact: sylvie.stucki@a3.epfl.ch, stephane.joost@epfl.ch

1 What is Samβada?

Samβada is an integrated software for landscape genomic analysis of large datasets. The key features are the study of local adaptation in relationship with environment and the measure of spatial autocorrelation in environmental and molecular datasets. On one hand, Samβada uses logistic regressions to estimate the probability that an individual carries a specific genetic marker given the habitat that characterises its sampling site. One the other hand, spatial autocorrelation is measured with Moran's I and local indicators of spatial association, in order to assess whether the observed data in each location depends on the values in the neighbouring locations. Underlying models are kept simple to put emphasis on process efficiency and user-available options.

2 Installation

Software, source code, documentation and examples are available on our webpage `lasig.epfl.ch/sambada`.

Executable binaires

Compiled versions of Samβada are already packaged for Windows, Mac OS and Ubuntu. Download and expand the archive at the location of your choice.

Compiling from sources

Just run `make` in the source folder, the executables are placed in the subfolder `binaries`.

Documentation

Software usage is explained in this manual. Theoretical background is covered by Samβada's release article [in preparation] and Joost et al. (2007). Extended information on methods and implementation can be found in Stucki (2014) (in French).

Examples

Three sample cases are provided with the software.

DataFromManual is a tiny set of six samples with fives environmental variables and seven molecular markers. The examples from this manual are build on this dataset in order to illustrate data format, analysis workflow and distributed computing.

RandomSample is a random set of 100 georeferenced points with two environmental variables and a molecular marker. The first environmental parameter is random, while the second one is correlated to longitude in order to provide some spatial autocorrelation. The molecular marker is random.

SubsetSNPCattle contains 386 SNPs from Ugandan cattle [lien approprié]. They are already recoded for Samβada, so there is three binary markers per loci. In this case, the spatial autocorrelation takes some time to compute.

Provided you have the file tree shown on fig. 1, if you launch a shell[1] and navigate to the folder `RandomData` or `SubsetCattleSNP`, examples can be run using:
`../../Binaries/Sambada.exe input-Sample100.txt Sample100.txt` or
`../../Binaries/Sambada.exe paramTest.txt TableEnvUG.csv extrait\_marq.txt`

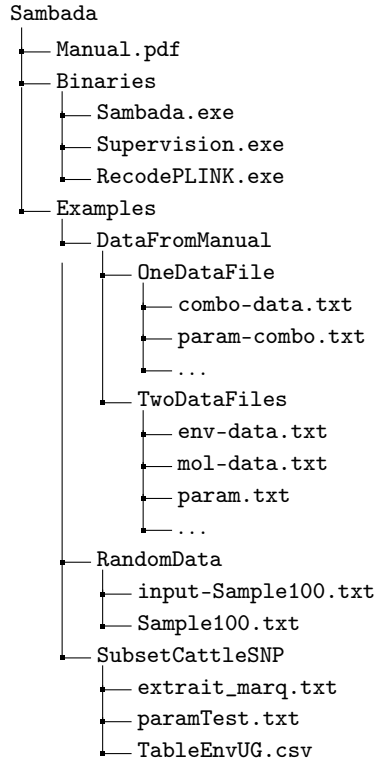


Figure 1 – Suggested file tree to run the examples.

[1] `Command Line` or `PowerShell` on Windows, `Terminal` on Mac OS and Linux, see p. 24.

3 Analysis overview

Three programs are available:

Samβada processes univariate and multivariate logistic models for the landscape genomics analysis and optionally measures the spatial autocorrelation in environmental and molecular datasets;

Supervision can split molecular data in blocks in order to run the analysis on several computers, and can merge the results afterwards;

RecodePLINK can translate molecular data from `PLINK`'s to Samβada's format.

The user must provide Samβada with a parameter file to set up the analysis as well as environmental and molecular data. The workflow is summarised on fig. 2 and the data format is presented in the next section.

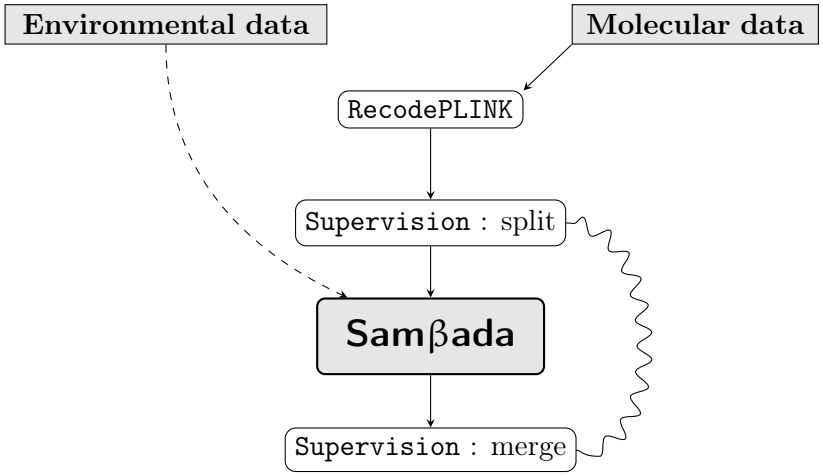


Figure 2 – Workflow of analysis. Rectangles stand for data and round-cornered figures stand for programs. Grey elements are mandatory and white ones are optional. Samβada computes correlative models and spatial autocorrelation. The two other features are optional: `Supervision` enables distributed computing while `RecodePLINK` transforms .ped/.map files to comply with Samβada's format. Arrows show processing order; Samβada input consists in environmental data (dashed line) and molecular data (solid line). The zigzag line indicates that `Supervision` is used before and after the main analysis.

4 Data format

Samβada's input consist of molecular and environmental data. They can be provided as a single or two separate files. Files may have any name and extension. Each line provides information for an individual, each column contains an environmental variable or a binary molecular marker. Examples are provided on fig. 3, 4 and 5. Information about data format and analysis options are specified separately in the parameter file.

Data files are organised as follows: the header line is optional and the column separator is up to the user. Sample names (identifiers) are optional, and some columns may be excluded from the analysis (for instance phenotypical information stored with the environmental data). If there is a single data file, environmental data must be provided in the first columns, and molecular data in the last ones. Sample names and coordinates are considered as environmental data. If data is split between two files, sample must be in the same order in both files. Missing data can be coded as any character string, for instance `NaN` or `?`. Fig. 3 and 4 are examples of environmental and molecular files. Fig. 5 is the combined file for the same data.

NAME	ENV1	ENV2	ENV3	ENV4	ENV5
ID1	46	972	236	230	132
ID2	32	987	238	232	83
ID3	32	987	238	232	83
ID4	32	987	NaN	232	83
ID5	32	987	238	232	83
ID6	35	1021	235	230	87

Figure 3 – Example of environmental file (`env-data.txt`).

NAME	M4	M7	M8	M9	M16	M17	M18
ID1	1	1	1	0	1	1	1
ID2	0	0	0	0	0	0	NaN
ID3	0	1	0	0	0	0	1
ID4	0	0	1	1	0	1	1
ID5	0	0	1	0	0	1	0
ID6	0	1	0	0	0	1	0

Figure 4 – Example of molecular file (`mol-data.txt`).

NAME	ENV1	ENV2	ENV3	ENV4	ENV5	M4	M7	M8	M9	M16	M17	M18
ID1	46	972	236	230	132	1	1	1	0	1	1	1
ID2	32	987	238	232	83	0	0	0	0	0	0	NaN
ID3	32	987	238	232	83	0	1	0	0	0	0	1
ID4	32	987	NaN	232	83	0	0	1	1	0	1	1
ID5	32	987	238	232	83	0	0	1	0	0	1	0
ID6	35	1021	235	230	87	0	1	0	0	0	1	0

Figure 5 – Example of combined file for environmental and molecular data, corresponding to fig. 3 and 4 (`combo-data.txt`). Environmental data must be provided in the first columns (left part of the tabular), and molecular data in the last columns (right part). The dentifier, if any, is considered as an environmental variable.

5 Program use

5.1 Samβada

5.1.1 Input files

The required input for Samβada consists of environmental and molecular data, formatted as explained in sec. 4. A parameter file is needed as well to set up the analysis.

The parameter file contains one line per parameter, they can be specified in any order. Each line begins with the name of the current parameter, followed by the values separated by spaces.

Some parameters are mandatory, otherwise the entire line may be omitted. Any line beginning with a hash character (#) will be ignored.

Fig. 6 presents a working parameter file.

Example 1 Let's assume we want to analyse `mol-data.txt` (fig. 4) with `env-data.txt` (fig. 3). The simplest parameter file is shown on fig. 7.

Example 2 When environmental and molecular data are provided altogether, slight changes in the parameter file reflect the new data size, see fig. 8.

5.1.2 Program launch

Samβada is launched as follows if environmental and molecular data are stored in the same file:

```
Sambada parameterFile dataFile
```

The command changes slightly if there are two separated input files:

```
  HEADERS YES
  WORDDELIM " "
* NUMVARENV 24
* NUMMARK 120103
* NUMINDIV 804
  IDINDIV short_name ID_indiv
  SPATIAL longitude latitude SPHERICAL NEAREST 20
  AUTOCORR BOTH MARK 1000
* DIMMAX 1
* SAVETYPE END BEST 0.01
```

Figure 6 – Example of a parameter file for setting up Samβada's analysis. Each line contains an option for the computation, those marked with a sign in the margin are mandatory. The line order has no influence. In this example, the two first lines indicate that data files contain a header line and that columns are separated by spaces. The next lines state the number of environmental variables, the number of molecular markers and the number of individuals/samples. The option `IDINDIV` indicates which columns contain identifiers of individuals; here environmental and molecular data are recorded in two separated files. The next two lines address the measure of the spatial autocorrelation, with the coordinates names, which are spherical, the weighting scheme and the bandwidth; here the 20 nearest neighbours are taken into account. The analysis will include both global and local autocorrelation (`BOTH`) of molecular markers (`MARK`) and the significance will be assessed with 1,000 permutations. The next option means that the detection of selection signatures will rely on univariate models (`DIMMAX 1`). The last ligne indicates that results will be stored at the end of the process, that only significant models with a significant parent will be stored and that the threshold for significance is set to 1% (before Bonferroni's correction).

```
HEADERS YES
NUMVARENV 6
NUMMARK 8
NUMINDIV 6
IDINDIV NAME
DIMMAX 1
SAVETYPE END ALL 0.01
```

Figure 7 – Parameter file to analyse data from fig. 3 and 4 (`param.txt`). `NUMVARENV` and `NUMMARK` count the total number of columns in the data files.

```
HEADERS YES
NUMVARENV 6
NUMMARK 7
NUMINDIV 6
IDINDIV NAME
DIMMAX 1
SAVETYPE END ALL 0.01
```

Figure 8 – Parameter file to analyse data from fig. 5 (`param-combo.txt`). Sample names are provided once, thus there is one molecular column less.

```
Sambada parameterFile envFile molecularFile
```

Therefore examples 1 and 2 would be launched with:
`Sambada param.txt env-data.txt mol-data.txt`
and
`Sambada param-combo.txt combo-data.txt`
respectively. Futher examples are provided on p. 3.

5.1.3 List of options

This section presents the available parameters for Samβada.

The options are presented in the following way: the first line shows the parameter name, whether it is mandatory, the list of possible values (or the expected type in parenthesis) and the default value. The paragraph is completed by a description of the option.

Data files and format

`INPUTFILE` Optional (string) -
Name(s) of the data file(s). If there are two files, indicate first the environmental file then the molecular file.
This information may also be given as an argument to the program.

`OUTPUTFILE` Optional (string) -
Base name(s) for the results file(s). If this option is omitted, the output files will be named after the molecular input file. The different ouput files are distinguished by adding suffixes ("-Out-", "-AS-", ...), thus the input files are untouched. With this option, the results can be saved in a different folder than the data.

`HEADERS` Optional Yes / No `No`

Presence or absence of variable names. If present, they are read on the first line of the data file, otherwise the environmental variables are labelled P1, P2, P3,... and molecular markers are labelled M1, M2, M3,....

`WORDDELIM` Optional (char) ‘ ’
Word delimiter, it must be a single character. This option applies to both molecular and environmental data, while the parameter file is assumed to be space-separated.

`LOG` Optional *1 value, see descr.* `BOTH`
Location of log information.

1
- TERMINAL / CONSOLE — print the log on the standard output,
- FILE — writes the log in a file with the suffix “-log”,
- BOTH — uses both methods.

Data size

`NUMVARENV` Mandatory (int) -
Number of columns with environmental variables, including ignored variables and the column of identifiers (if any). If there is one input file, this counts the number of columns that don't concern molecular data[2]. If there are two input files, NUMVARENV counts the total number of columns in the environmental data file.

`NUMMARK` Mandatory (int) -
Number of columns with molecular data, including ignored data and identifiers if applicable. If there is one input file, this counts the number of columns concerning molecular markers[2]. If there are two input files, NUMMARK counts the total number of columns in the molecular data file.
For distributed analysis, this parameter must indicate the number of markers for the current block of data followed by the total number of markers[3].

[2]In this case, NUMVARENV + NUMMARK is the total number of columns in the molecular data file. The first NUMVARENV columns contain environmental data and the following NUMMARK columns hold molecular markers.

[3]The total number of markers is used to compute the Bonferroni correction. Thus ignored data should be excluded of this total.

`NUMINDIV` Mandatory (int) -
Number of samples included in the data file(s).

Active and inactive columns

`IDINDIV` Optional (string or int) -
Name(s) of the column(s) containing sample identifiers[4]. These optional identifiers are used to label samples in the output files for local spatial autocorrelation (otherwise the line numbers are used). If there are two data files, two names (or numbers) can be provided, the first one is for the environmental data and the second one is for molecular data. The identifier columns are automatically set as inactive. Moreover if this option is specified with two data files, the two identifiers must match on each line. (Sample must be in the same order in each file.)

`COLSUPENV` Optional (string or int) -
Name(s) of the column(s) in the environmental data to be excluded from the analysis[4]. These columns are set as inactive. (For instance, COLSUPENV can indicate columns such as the sampling date or the name of the area.)

`COLSUPMARK` Optional (string or int) -
Name(s) of the column(s) in the molecular data to be excluded from the analysis[4]. These columns are set as inactive.

`SUBSETVARENV` Optional (string or int) -
Name(s) of the column(s) in the environmental data to be included in the analysis while the other columns are set as inactive. The different options cumulate: the active columns are those listed here, minus those specified with COLSUPENV as well as IDINDIV.

`SUBSETMARK` Optional (string or int) -
Name(s) of the column(s) in the molecular data to be included in the analysis while the other columns are set as inactive. The different options cumulate: the active columns are those listed here, minus those specified with COLSUPMARK as well as IDINDIV.

[4]The column numbers replace their names in case there is no header line.

Logistic model and results storage.

`DIMMAX` Mandatory (int) -
Maximum number of environmental variables included in the logistic models. The models with less parameters are computed as well. Use 1 for univariate models, 2 for univariate and bivariates models...

`SAVETYPE` Mandatory *3 values, see descr.* -
Saving method and model selection.

1	REAL END	Storage mode: REAL saves results during processing, END writes them upon completion of computation. The second option enables sorting the models according to their Wald scores before saving.
2	ALL SIGNIF BEST	Model selection: ALL saves all models, SIGNIF saves significant models (according to the G and Wald scores) and BEST saves significant models with at least a significant parent.
3	(double)	Significance threshold (p-value) for options SIGNIF and BEST. The Bonferroni correction is applied on this threshold.

Example: `SAVETYPE END BEST 0.01`

`UNCONVERGEDMODELS` Optional Yes / No `No`
This option controls the back-up of unconverged models. If enabled, these models are saved in a separate file with the suffix "-unconvergedModels".

Spatial autocorrelation

`SPATIAL` Optional *5 values, see descr.* -

1	(string or int)	Column name (or number) for longitude.
2	(string or int)	Column name (or number) for latitude.
3	SPHERICAL CARTESIAN	Type of coordinates (spherical or projected).
4	DISTANCE GAUSSIAN BISQUARE NEAREST	Type of weighting scheme, see fig. 9
5	(double or int)	Bandwidth of the weighting function (double for the first three cases (in km), int for the last).

Example: `SPATIAL X Y CARTESIAN BISQUARE 10`

`AUTOCORR` Optional *3 values, see descr.* -

This entry requires the specification of SPATIAL.

1	GLOBAL LOCAL BOTH	Type of indices to compute: Moran's I for the global spatial autocorrelation, LISA for the local one.
2	ENV MARK BOTH	Variables for the analysis.
3	(int)	Number of permutations for computing the pseudo p-values (default=99).

Example: `AUTOCORR GLOBAL BOTH 999`

`SHAPEFILE` Optional YES / NO `NO`

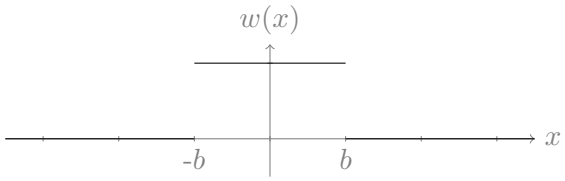
With this option, the LISA are saved as a shapefile (in addition to the usual output). This format is composed of three files: .shp, .shx and .bdf. These files can be loaded together in any GIS software to map the local autocorrelation. This entry requires the specification of SPATIAL.

5.1.4 Output

Samβada produces several output files. To illustrate the naming scheme, let us assume that the molecular data file is named `data.ext`. If the log is saved for future reference, the corresponding file is named `data-log.ext`. For logistic regressions, there is one file for constant models, which are not sorted (see fig. 11). There is also one file per distinct number of parameters (univariate, bivariate, trivariate models and so on, see fig. 12). In these files, models are

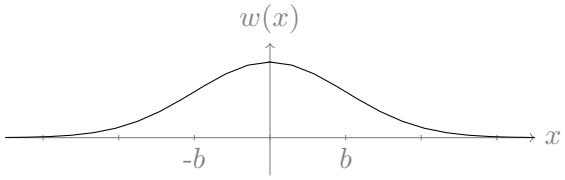
Moving window

$$w_{ij} = \begin{cases} 1 & \text{if } d_{ij} < b \\ 0 & \text{otherwise} \end{cases}$$



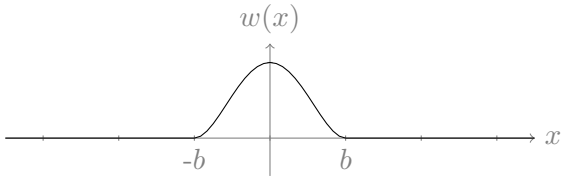
Gaussian kernel

$$w_{ij} = \exp\left[-\frac{1}{2}\left(\frac{d_{ij}}{b}\right)^2\right]$$



Bisquare kernel

$$w_{ij} = \begin{cases} \left[1 - \left(\frac{d_{ij}}{b}\right)^2\right]^2 & \text{if } d_{ij} < b \\ 0 & \text{otherwise} \end{cases}$$



N nearest neighbours

$$w_{ij} = \begin{cases} \frac{1}{N} & \text{if } j \text{ is amongst the } N \text{ nearest neighbours of } i \\ 0 & \text{otherwise} \end{cases}$$

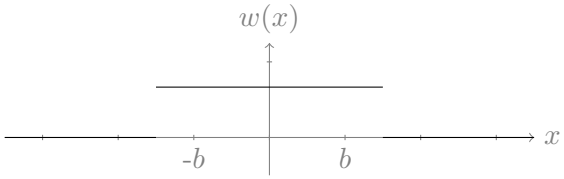


Figure 9 – Weighting schemes available for measuring spatial autocorrelation.

sorted according to their Wald scores. Fig. 10 lists possible errors for logistic models. If the back-up of unconverged models is enabled, the output file is named `data-unconvergedModels.ext`. Results files are named as follows: constant models are saved in the file `data-Out-0.ext`, univariate models in the file `data-Out-1.ext`, bivariate models the file `data-Out-2.ext`, and so on.

0 Success
1 Exponential divergence ($\boldsymbol{X\beta}$ is diverging)
2 Singular matrix (impossible to invert the information matrix)
3 Too large $\boldsymbol{\beta}$ (divergence)
4 Maximal number of iteration number reached without convergence
5 Monomorphic marker (appears in the output file for constant models)
6 Significant model with non-significant parents (multivariate analysis with option `SIGNIF`)

Figure 10 – List of possible errors for logistic models.

Marker	Loglikelihood	AverageProb	Beta_0	NumError
Hapmap43437-BTA-101873_AA	-228.2100569	0.082089552	-2.414289083	0
Hapmap43437-BTA-101873_AG	-542.450042	0.404228856	-0.387875415	0
Hapmap43437-BTA-101873_GG	-556.9893006	0.513681592	0.054740033	0
ARS-BFGL-NGS-16466_AA	-44.84132815	0.009950249	-4.600157644	0
ARS-BFGL-NGS-16466_AG	-389.8189189	0.189054726	-1.456164041	0
ARS-BFGL-NGS-16466_GG	-401.2120224	0.800995025	1.392524911	0
Hapmap34944-BES1_Contig627_1906_AA	-456.4590694	0.254975124	-1.072251619	0
Hapmap34944-BES1_Contig627_1906_AC	-555.856645	0.470149254	-0.119545151	0
Hapmap34944-BES1_Contig627_1906_CC	-472.7907257	0.274875622	-0.970024485	0

Figure 11 – Exemple of Samβada's results for constant models, there is one marker per line. The first column is the name of the molecular marker, here the locus name combined with the allele name. The following columns are the log-likelihood, the frequency of the marker, the estimate of parameter β_0 for the logistic model and the error code (0 if success). Constant models are not sorted and thus are in the same order as the markers in the input file. When considered markers are SNPs like here, there are three binary markers per locus.

Concerning the measure of spatial autocorrelation, results are stored separately for environmental data and molecular markers. In each case, there are three output files. The first one is named `Data-AS-Env.ext` (or `Data-AS-Mark.ext`) and stores Moran's I and local indicators of spatial association (Anselin, 1995). If provided, the sample names appear in the first column. If both Moran's I and LISAs are computed, the first line is the global index and each subsequent line is a local index, samples are in the same order as in the data file. The second file is either named `Data-AS-Env-Sim.ext` (or `Data-AS-Mark-Sim.ext`) and stores the simulated values of the global

Marker	Env_1	Loglikelihood	Gscore	WaldScore	NumError	Efron	McFadden	McFaddenAdj	CoxSnell	Nagelkerke	AIC	BIC	Beta_0	Beta_1
Hapmap41074-BTA-73520_AA	prec7	-443.11	208.53	151.72	0	0.25	0.19	0.19	0.23	0.10	890.22	912.98	-2.04	0.03
ARS-BFGL-NGS-113888_GG	prec7	-441.73	208.67	151.70	0	0.25	0.19	0.19	0.23	0.10	887.47	910.23	-2.02	0.03
Hapmap41762-BTA-117570_GG	prec7	-435.96	202.93	148.43	0	0.24	0.19	0.19	0.22	0.10	875.92	898.68	-1.86	0.03
ARS-BFGL-NGS-46098_GG	prec7	-440.04	200.82	147.60	0	0.24	0.19	0.18	0.22	0.10	884.07	906.83	-1.88	0.03
ARS-BFGL-NGS-113888_GG	latitude	-449.13	193.89	146.89	0	0.23	0.18	0.17	0.21	0.09	902.25	925.01	-0.73	0.86
Hapmap41074-BTA-73520_AA	latitude	-450.81	193.13	146.61	0	0.23	0.18	0.17	0.21	0.09	905.62	928.38	-0.75	0.85
Hapmap41762-BTA-117570_GG	latitude	-444.40	186.04	141.99	0	0.21	0.17	0.17	0.21	0.09	892.80	915.56	-0.57	0.84
ARS-BFGL-NGS-113888_GG	prec6	-455.48	181.19	138.85	0	0.21	0.17	0.16	0.20	0.09	914.95	937.71	-2.22	0.03
Hapmap41074-BTA-73520_AA	prec6	-457.38	179.99	138.13	0	0.21	0.16	0.16	0.20	0.09	918.77	941.53	-2.23	0.03
ARS-BFGL-NGS-46098_GG	latitude	-451.22	178.45	138.11	0	0.21	0.17	0.16	0.20	0.09	906.44	929.20	-0.59	0.82
Hapmap41813-BTA-27442_AA	prec7	-462.30	179.89	137.52	0	0.22	0.16	0.16	0.20	0.08	928.60	951.36	-1.92	0.03
ARS-BFGL-NGS-46098_GG	prec6	-451.51	177.87	137.27	0	0.21	0.16	0.16	0.20	0.09	907.03	929.78	-2.11	0.03
BTA-73516-no-rs_AA	prec7	-460.18	177.43	136.04	0	0.21	0.16	0.16	0.20	0.08	924.35	947.11	-1.83	0.03
Hapmap41813-BTA-27442_AA	latitude	-469.89	164.71	130.98	0	0.20	0.15	0.15	0.19	0.08	943.77	966.53	-0.76	0.76
Hapmap41762-BTA-117570_GG	prec6	-454.17	166.51	130.97	0	0.20	0.15	0.15	0.19	0.08	912.33	935.09	-1.96	0.03
ARS-BFGL-NGS-46098_GG	longitude	-458.86	163.18	130.95	0	0.18	0.15	0.15	0.18	0.08	921.72	944.48	-23.95	0.76
Hapmap41074-BTA-73520_AA	bio7	-457.07	180.61	129.73	0	0.21	0.16	0.16	0.20	0.09	918.14	940.90	-11.85	0.08
ARS-BFGL-NGS-113888_GG	bio7	-456.32	179.50	128.90	0	0.20	0.16	0.16	0.20	0.09	916.64	939.40	-11.82	0.08
BTA-73516-no-rs_AA	latitude	-468.36	161.06	128.61	0	0.19	0.15	0.14	0.18	0.08	940.72	963.48	-0.67	0.76
Hapmap28985-BTA-73836_CC	prec6	-457.78	157.45	125.68	0	0.19	0.15	0.14	0.18	0.08	919.57	942.33	1.87	-0.03
Hapmap31863-BTA-27454_GG	prec7	-474.85	155.28	123.46	0	0.19	0.14	0.14	0.18	0.07	953.70	976.43	-1.91	0.02
ARS-BFGL-NGS-46098_GG	bio7	-456.70	167.50	121.71	0	0.20	0.15	0.15	0.19	0.08	917.39	940.15	-11.35	0.08
BTA-73516-no-rs_AA	prec6	-474.90	147.99	119.50	0	0.17	0.13	0.13	0.17	0.07	953.79	976.55	-1.97	0.03
Hapmap41762-BTA-117570_GG	bio7	-460.77	153.30	113.69	0	0.18	0.14	0.14	0.17	0.07	925.54	948.30	-10.71	0.07
Hapmap28985-BTA-73836_GG	bio3	-381.27	160.94	111.21	0	0.21	0.17	0.17	0.18	0.10	766.54	789.30	19.98	-0.26
ARS-BFGL-NGS-113888_GG	bio3	-471.77	148.61	106.51	0	0.17	0.14	0.13	0.17	0.07	947.53	970.29	20.21	-0.24

Figure 12 – Exemple of Samβada's results for univariate models, there is one marker per line. The first column is the name of the molecular marker, here the locus name combined with the allele name. The second column is the name of the environmental variable. The following columns are the log-likelihood, G score, Wald score and the error code (0 if success). The five next columns are goodness-of-fit measures for the regression (pseudo-R^2). The analysis includes the AIC (*Akaike information criterion*) and BIC (*Bayesian information criterion*) as well. The two last column contain the parameters β for the regression, one constant parameter and one corresponding to the environmental variable. Results file for multivariate models contain additional columns for environmental variables (Env_2, Env_3, ...) and for regression parameters (Beta_2, Beta_3, ...).

Moran's I for each variable. This file can be used to plot their distribution and compare it to the actual value of the index. Simulation results are not stored for LISAs in order to save disk space. The third file is named `Data-AS-Env-pVal.ext` (or `Data-AS-Mark-pVal.ext`) and stores the pseudo p-values for the permutations-based significance tests. For R permutations and M events "I_{sim} is equal or more extreme than I", the p-value is $\frac{M+1}{R+1}$.

If requested, LISAs are also stored as a shapefile whose parts are named `data.shp`, `data.shx` and `data.dbf` (for data file `data.ext`). This format is read by any GIS software, for instance `QuantumGIS`[5].

5.2 `Supervision`

For large molecular datasets, computation workload may be distributed among several computers. To this end, `Supervision` is called prior to the analysis to split the molecular dataset in blocks (see fig. 13). The new files are named automatically on the basis of the molecular data file. The last file will contain less markers if the total number is not divisible by the block size. Each share of data is processed separately, either on the same multicore computer or on distrinct computers. Environmental data must provided to each processing node. Results are gathered afterwards so `Supervision` can merge them and produce the same output as if the whole analysis were run on a single node.

5.2.1 Split process

Information about splitting are provided by a parameter file and the processed is launched as follow:

```
Supervision parameterFile
```

The parameter file must contain the six following lines (in the same order):

`dataFile`	name of the data or molecular file (beware of trailing tabulations)
`paramFile`	name of the parameter file (not used yet)
`numEnv`	number of environmental parameters*
`numMark`	number of molecular markers
`numLines`	number of lines in the data file
`blockSize`	size of blocks of molecular data

Figure 14 – Instance of parameter file for `Supervision`.

*`numEnv` indicates the number of non-molecular columns in the file to be recoded. These variables will be copied to a separate file. If the molecular file contains no ID or environmental column, `numEnv` is to be set to 0. Please

[5] `www.qgis.org`

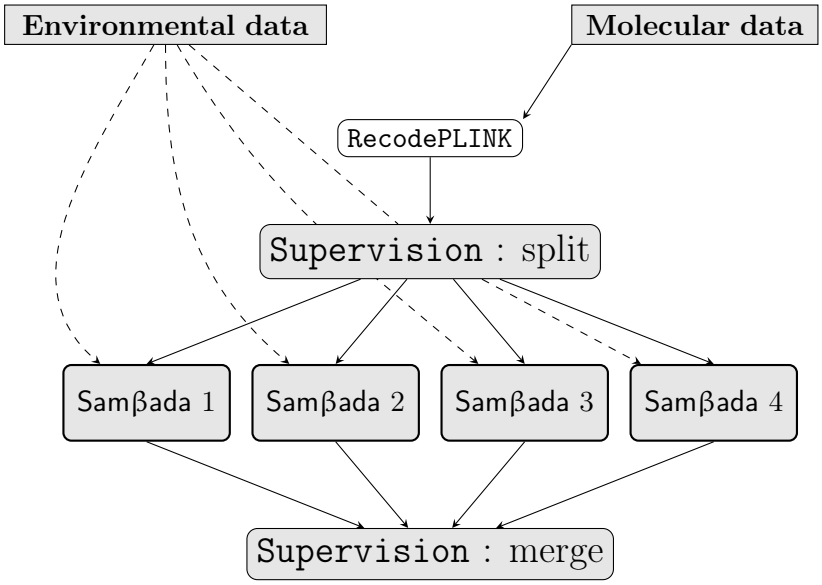


Figure 13 – Workflow of analysis for distributed computing. Rectangles stand for data and round-cornered figures stand for programs. Grey elements are mandatory and white ones are optional. Arrows show processing order for environmental data (dashed line) and for molecular data (solid line). `Supervision` is used before Samβada to split molecular data in blocks and afterwards to merge results.

also note that the fifth parameter counts the total number of lines, including the header line if any.

New data files are named automatically. The molecular file names contains two numbers, the first one is the block number (starting from 0) and the second one is the number of the first marker in the block (starting from 0 in the first block).

Example 1 Let's assume the data of fig. 4 is stored in `mol-data.txt` and that we want blocks of four markers. The corresponding parameter file is shown on fig. 15 and the splitting is performed as follows:
`Supervision param-split.txt`
The resulting data files (`mol-data-env.txt`, `mol-data-mark-0-0.txt` and `mol-data-1-4.txt`) are displayed on fig. 16.

```
mol-data.txt
thingy.txt
1                numEnv
7                numMark
7                numLines
4                blockSize
```

Figure 15 – Parameter file for `Supervision` in case molecular data of fig. 4 is stored in `mol-data.txt` and is to be split in blocks of four markers.

NAME
ID1
ID2
ID3
ID4
ID5
ID6

(a) File `mol-data-env.txt`

M4	M7	M8	M9
1	1	1	0
0	0	0	0
0	1	0	0
0	0	1	1
0	0	1	0
0	1	0	0

(b) File `mol-data-mark-0-0.txt`

M16	M17	M18
1	1	1
0	0	NaN
0	0	1
0	1	1
0	1	0
0	1	0

(c) File `mol-data-mark-1-4.txt`

Figure 16 – Molecular data of fig. 4 after splitting in block of four markers.

In this case, the column NAME is considered as an environmental variable (since it is not a molecular marker). NAME will be copied to the file `mol-data-env.txt` which will not be used for Samβada's analysis. The actual environmental data (`env-data.txt`) is shown on fig. 3. The column

NAME cannot be used as an identifier since it was not copied to the molecular data. Thus it must be indicated as a supplementary column to Samβada (option COLSUPENV, see p. 10).

Example 2 `Supervision` can split combined data files, containing both environmental and molecular information. Figure 17 shows the parameter file used to split data from fig. 5 (stored in `combo-data.txt`) in blocks of three markers. The splitting is performed as follows:
`Supervision param-split-combo.txt`
The data files will be named `combo-data-env.txt`, `combo-data-mark-0-0.txt`, `combo-data-mark-1-3.txt` and `combo-data-mark-2-6.txt`, the latter will have only one column (see fig. 18). In this case, `combo-data-env.txt` will contain environmental data and can be used in Samβada's analysis. As in the previous example, the column NAME cannot be used as an identifier since it was not copied to the molecular data. Thus it must be indicated as a supplementary column to Samβada (option COLSUPENV, see p. 10).

```
combo-data.txt
thingy.txt
6          numEnv
7          numMark
7          numLines
3          blockSize
```

Figure 17 – Parameter file for `Supervision` in case molecular data of fig. 5 is stored in `combo-data.txt` and is to be split in blocks of three markers.

5.2.2 Analysis with Samβada

The distributed analysis follows the same process as the single-node one. The parameter file has to be modified to include both the current and the total number of molecular markers (parameter `NUMMARK`, see p. 9). Thus if the last block has less markers than the other ones, there will be a common parameter file for the first blocks and another one for the last block. The total number of markers is used to adjust the significance threshold with the Bonferroni correction (if relevant).

Example 1 Fig. 19 shows the parameter files needed to analyse molecular data from fig. 16 (b and c) with environmental data from fig. 3. For comparison, the parameter file for single node analysis is shown on fig. 7. Beside the change in the number of markers, the column NAME has to be indicated as supplementary data (COLSUPENV) since it is not available in the molecular files.

NAME	ENV1	ENV2	ENV3	ENV4	ENV5
ID1	46	972	236	230	132
ID2	32	987	238	232	83
ID3	32	987	238	232	83
ID4	32	987	NaN	232	83
ID5	32	987	238	232	83
ID6	35	1021	235	230	87

(a) File `mol-data-env.txt`

M4	M7	M8
1	1	1
0	0	0
0	1	0
0	0	1
0	0	1
0	1	0

(b) File `combo-data-mark-0-0.txt`

M9	M16	M17
0	1	1
0	0	0
0	0	0
1	0	1
0	0	1
0	0	1

(c) File `combo-data-mark-1-3.txt`

M18
1
NaN
1
1
0
0

(d) File `combo-data-mark-2-6.txt`

Figure 18 – Molecular data of fig. 5 after splitting in blocks of three markers.

```
HEADERS YES
NUMVARENV 6
NUMMARK 4 7
NUMINDIV 6
COLSUPENV NAME
DIMMAX 1
SAVETYPE END ALL 0.01
```

(a) `param-a.txt`

```
HEADERS YES
NUMVARENV 6
NUMMARK 3 7
NUMINDIV 6
COLSUPENV NAME
DIMMAX 1
SAVETYPE END ALL 0.01
```

(b) `param-b.txt`

Figure 19 – Parameter files for distributed analysis with Samβada. File `param-a.txt` is used for data from fig. 3 and 16b. Usually there are more blocks of molecular data, and all blocks containing the same number of markers would be analysed with this set of parameters. File `param-b.txt` is used for the last block of molecular data, when it contains less markers (data from fig. 3 and 16c).

The analysis is launched with two commands:

```
Sambada param-a.txt env-data.txt mol-data-mark-0-0.txt
Sambada param-b.txt env-data.txt mol-data-mark-1-4.txt
```

Example 2 Fig. 20 shows the parameter files needed to analyse molecular data from fig. 18 (b, c and d) with environmental data from fig. 18a. For comparison, the parameter file for single node analysis is shown on fig. 8. Beside the change in the number of markers, the column NAME has to be indicated as supplementary data (COLSUPENV) since it is not available in the molecular files.

```
HEADERS YES
NUMVARENV 6
NUMMARK 3 7
NUMINDIV 6
COLSUPENV NAME
DIMMAX 1
SAVETYPE END ALL 0.01
```

(a) `param-combo-a.txt`

```
HEADERS YES
NUMVARENV 6
NUMMARK 1 7
NUMINDIV 6
COLSUPENV NAME
DIMMAX 1
SAVETYPE END ALL 0.01
```

(b) `param-combo-b.txt`

Figure 20 – Parameter files for distributed analysis with Samβada. Data file `combo-data.txt` has been split in fig. 18, all computations use environmental data from subfig. *a*. File `param-combo-a.txt` is used to analyse markers from subfig. *b* and *c*, while file `param-combo-b.txt` is used for the last block of molecular data (subfig. *d*).

The analysis is launched with three commands:

```
Sambada param-combo-a.txt combo-data-env.txt combo-data-mark-0-0.txt
Sambada param-combo-a.txt combo-data-env.txt combo-data-mark-1-3.txt
Sambada param-combo-b.txt combo-data-env.txt combo-data-mark-2-6.txt
```

5.2.3 Merge process

Once all blocks of markers have been analysed with Samβada, `Supervision` can merge the results. Copy every output file (whose name contains `"-Out-"`) to a single folder, then launch the program as follows:

```
Supervision base-name.txt numBlock blockSize maxDimension
```

`base-name.txt` is the name of the molecular or combined data file which was split in blocks. `numBlocks` and `blockSize` refer to the number of data blocks (including the last one) and to the size of the "complete" ones. `maxDimension` is the maximum number of environmental parameters included in the models (1 for univariate analysis, 2 for bivariate analysis, ...)

`Supervision` merges all results, discards unconverged models (error numbers 1-5) and sort models according to their Wald score. One output file is produced for each dimension of modeling, as in the single-node Samβada's analysis. If the original data file is called `base-name.txt`, the results files are named `base-name-res-0.txt`, `base-name-res-1.txt`, `base-name-res-2.txt`, ...

Example 1 Data file `mol-data.txt` was split in two blocks of four markers and the analysis involved univariate models:

```
Supervision mol-data.txt 2 4 1
```

Example 2 Data file `combo-data.txt` was split in three blocks of three markers and the analysis involved univariate models:

```
Supervision combo-data.txt 3 3 1
```

`Supervision` also takes some optional arguments. The complete call is:

```
Supervision base-name.txt numBlock blockSize maxDimension ···
   selScore scoreThreshold sortScore wordDelim
```

`selScore` indicates which score(s) is/are used to select significant models; possible values are `G`, `Wald` and `BOTH` (the default). `scoreThreshold` indicates the minimum score for which a model is considered as significant. This option can be used either to apply Bonferroni correction when all models were saved during the analysis or to select a subset of models, for instance for a post-processing analysis in `R`. `selScore` and `scoreThreshold` must

be provided together. `sortScore` indicates which score is used to sort the models; possibles values are `G`, `Wald` (the default), `AIC` and `BIC`. `wordDelim` shows the current word delimiter (space is the default).

Optional arguments may be omitted from right to left. Thus the possible sets of arguments are:

```
Supervision base-name.txt numBlock blockSize maxDimension
```

```
Supervision base-name.txt numBlock blockSize maxDimension ···
   selScore scoreThreshold
```

```
Supervision base-name.txt numBlock blockSize maxDimension ···
   selScore scoreThreshold sortScore
```

```
Supervision base-name.txt numBlock blockSize maxDimension ···
   selScore scoreThreshold sortScore wordDelim
```

5.3 RecodePLINK

This tools allows the recoding of PLINK's `.ped` and `.map` files to Samβada's format (see Purcell, 2009, for further information on this format). `RecodePLINK` is called as follows:
`RecodePLINK nbSamples nbSNPs inputFile outputFile`
In case only a subset of the samples are to be used, the list of sample names may be provided in a separate file (one name per line):
`RecodePLINK nbSamples nbSNPs inputFile outputFile subsetFile`
Please note that RecodePLINK does not recognise comment lines in `.ped`/`.map` files at the moment. Please remove them before recoding.

6 Frequently Asked Questions

I am lost with the Command Line!

Don't panic, there are a couple of online tutorials. For Windows, you can start with `http://www.cs.princeton.edu/courses/archive/spr05/cos126/cmd-prompt.html`. (Hint: Use `PowerShell` instead of the `Command Line`.)

Mac OS and Linux `Terminal` are basically the same, see for instance: `http://www.davidbaumgold.com/tutorials/command-line/`.

My results do not make any sense!

Check whether the samples in the environmental data are in the same order as those in the molecular data. What could have happened is that one of your files got sorted by some column during data preparation.

To be continued...

References

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